

Exhibit X



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

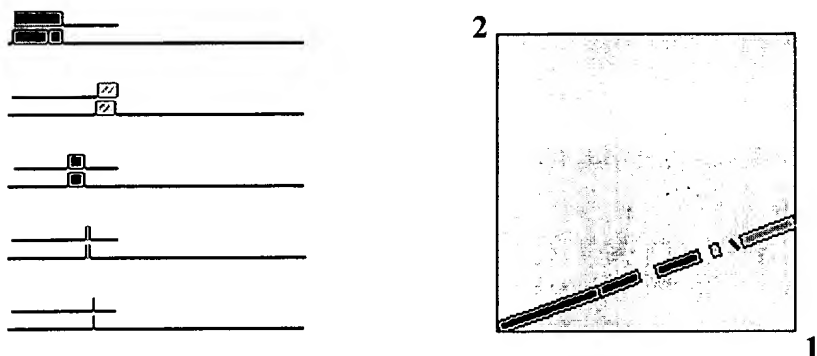
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: Mismatch: gap open: gap extension: x_dropoff: expect: wordsize: Filter ☒ View option Masking character option Masking color option ☐ Show CDS translation Sequence 1: [gi|4454551|gb|AF113003.1|AF113003](#) SEQ ID NO: 4

Length = 3094 (1 .. 3094)

Sequence 2: [gi|4559297|gb|AF125672.1|AF125672](#)

Length = 8686 (1 .. 8686)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 2680 bits (1394), Expect = 0.0
 Identities = 1465/1480 (98%), Gaps = 3/1480 (0%)
 Strand=Plus/Plus

Query	1	CATGTCGGGCTCCACACAGCTTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGCTACCC	60
Sbjct	156	CATGTCGGGCTCCACACAGCCTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGCTACCC	215
Query	61	GCCCCACAGCCTTTTCCTACCCAGTGCAGATCGCCCGGACGCACACGGACGTCGGGCTCCT	120
Sbjct	216	GCCCCACAGCCTTTTCCTACCCAGTGCAGATCGCCCGGACGCACACGGACGTCGGGCTCCT	275
Query	121	GGAGTACCAGCACCCTCCCGCGACTATGCCTCCACCTGTCGCCGGGCTCCATCATCCA	180

Sbjct	276	 GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	181	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	181	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	336	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	241	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	396	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	301	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	456	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	361	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	516	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	421	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	576	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	481	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	636	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	541	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	696	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	601	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	756	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	661	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	816	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	721	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	876	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	781	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	936	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	841	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	996	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	901	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	1056	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	961	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Sbjct	1116	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335
Query	1021	GGAGTACCAGCACCACCTCCCGCGACTATGCCTCCACCTGTCGCCCCGGCTCCATCATCCA	335

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Sbjct  1176  |||||
          CCGCAAGCAGCGCGAGCTGCAGGAGCGCATGCAG---AGGGTGGGCCAGCGGGGCAGTGG 1232
Query  1081  GCTGTCCATGTCGCGCCGCCCGCAGCGAGCACGAGGTGTCAGAGATCATCGATGGCCTCTC 1140
          |||||
Sbjct  1233  GCTGTCCATGTCGCGCCGCCCGCAGCGAGCACGAGGTGTCAGAGATCATCGATGGCCTCTC 1292
Query  1141  AGAGCAGGAGAACCTGGAGAAGCAGATGCGCCAGCTGGCCGTGATCCCGCCCATGCTGTA 1200
          |||||
Sbjct  1293  AGAGCAGGAGAACCTGGAGAAGCAGATGCGCCAGCTGGCCGTGATCCCGCCCATGCTGTA 1352
Query  1201  CGACGCTGACCAGCAGCGCATCAAGTTCATCAACATGAACGGGCTTATGGCCGACCCCAT 1260
          |||||
Sbjct  1353  CGACGCTGACCAGCAGCGCATCAAGTTCATCAACATGAACGGGCTTATGGCCGACCCCAT 1412
Query  1261  GAAGGTGTACAAAGACCGCCAGGTCATGAACATGTGGAGTGAGCAGGAGAAGGAGACCTT 1320
          |||||
Sbjct  1413  GAAGGTGTACAAAGACCGCCAGGTCATGAACATGTGGAGTGAGCAGGAGAAGGAGACCTT 1472
Query  1321  CCGGGAGAAGTTCATGCAGCATCCCAAGAACTTTGGCCTGATCGCATCATTCCTGGAGAG 1380
          |||||
Sbjct  1473  CCGGGAGAAGTTCATGCAGCATCCCAAGAACTTTGGCCTGATCGCATCATTCCTGGAGAG 1532
Query  1381  GAAGACAGTGGCTGAGTGCGTCCTCTATTACTACCTGACTAAGAAGAATGAGAACTATAA 1440
          |||||
Sbjct  1533  GAAGACAGTGGCTGAGTGCGTCCTCTATTACTACCTGACTAAGAAGAATGAGAACTATAA 1592
Query  1441  GAGCCTGGTGAGACGGAGCTATCGGCGCCGCGGCAAGAGC 1480
          |||||
Sbjct  1593  GAGCCTGGTGAGACGGAGCTATCGGCGCCGCGGCAAGAGC 1632

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Score = 1013 bits (527), Expect = 0.0
Identities = 561/564 (99%), Gaps = 0/564 (0%)
Strand=Plus/Plus

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Query  2531  AAGCCCCCGCGGCTGAGGAGCTGGCAGTGGACACAGGGAAGGCCGAGGAGCCCGTCAAG 2590
          |||||
Sbjct  2632  AAGCCCCCGCGGCTGAGGAGCTGGCAGTGGACACAGGGAAGGCCGAGGAGCCCGTCAAG 2691
Query  2591  AGCGAGTGCACGGAGGAAGCCGAGGAGGGGCCGCGCAAGGGCAAGGACGCGGAGGCCGCT 2650
          |||||
Sbjct  2692  AGCGAGTGCACGGAGGAAGCCGAGGAGGGGCCGCGCAAGGGCAAGGACGCGGAGGCCGCT 2751
Query  2651  GAGGCCACGGCCGAGGGGGCGCTCAAGGCAGAGAAGAAGGAGGGCGGGAGCGGCAGGGCC 2710
          |||||
Sbjct  2752  GAGGCCACGGCCGAGAGGGCGCTCAAGGCAGAGAAGAAGGAGGGCGGGAGCGGCAGGGCC 2811
Query  2711  ACCACTGCCAAGAGCTCGGGCGCCCCCAGGACAGCGACTCCAGTGCTACCTGCAGTGCA 2770
          |||||
Sbjct  2812  ACCACAGCCAAGAGCTCGGGCGCCCCCAGGACAGCGACTCCAGTGCCACCTGCAGTGCA 2871
Query  2771  GACGAGGTGGATGAGGCCGAGGGCGGCGACAAGAACCGGCTGCTGTCCCCAAGGCCCAGC 2830
          |||||
Sbjct  2872  GACGAGGTGGATGAGGCCGAGGGCGGCGACAAGAACCGGCTGCTGTCCCCAAGGCCCAGC 2931

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Query	2831	CTCCTCACCCCGACTGGCGACCCCGGGCCAATGCCTCACCCAGAAAGCCACTGGACCTG	2890
Sbjct	2932	CTCCTCACCCCGACTGGCGACCCCGGGCCAATGCCTCACCCAGAAAGCCACTGGACCTG	2991
Query	2891	AAGCAGCTGAAGCAGCGAGCGGCTGCCATnnnnnnnnATCCAGGTCACCAAAGTCCATGAG	2950
Sbjct	2992	AAGCAGCTGAAGCAGCGAGCGGCTGCCATCCCCCATCCAGGTCACCAAAGTCCATGAG	3051
Query	2951	nnnnnnnnGGGAGGACGCAGCTCCCACCAAGCCAGCTCCCCAGCCCCACCGCCACCGCAA	3010
Sbjct	3052	CCCCCGGGGAGGACGCAGCTCCCACCAAGCCAGCTCCCCAGCCCCACCGCCACCGCAA	3111
Query	3011	AACCTGCAGCCGGAGAGCGACGCCCTCAGCAGCCTGGCAGCAGCCCCGGGGCAAGAGC	3070
Sbjct	3112	AACCTGCAGCCGGAGAGCGACGCCCTCAGCAGCCTGGCAGCAGCCCCGGGGCAAGAGC	3171
Query	3071	AGGAGCCCGGCACCCCGCCGAC	3094
Sbjct	3172	AGGAGCCCGGCACCCCGCCGAC	3195

Score = 898 bits (467), Expect = 0.0
Identities = 467/467 (100%), Gaps = 0/467 (0%)
Strand=Plus/Plus

Query	1633	CCTCCTCAAGGAGAAGACAGACGACACCTCAGGGGAGGACAACGACGAGAAGGAGGCTGT	1692
Sbjct	1785	CCTCCTCAAGGAGAAGACAGACGACACCTCAGGGGAGGACAACGACGAGAAGGAGGCTGT	1844
Query	1693	GGCCTCCAAAGGCCGAAAACCTGCCAACAGCCAGGGAAGACGCAAAGGCCGCATCACCCG	1752
Sbjct	1845	GGCCTCCAAAGGCCGAAAACCTGCCAACAGCCAGGGAAGACGCAAAGGCCGCATCACCCG	1904
Query	1753	CTCAATGGCTAATGAGGCCAACAGCGAGGAGGCCATCACCCCCAGCAGAGCGCCGAGCT	1812
Sbjct	1905	CTCAATGGCTAATGAGGCCAACAGCGAGGAGGCCATCACCCCCAGCAGAGCGCCGAGCT	1964
Query	1813	GGCCTCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAAGAAGAAATGGAAACAGCCAA	1872
Sbjct	1965	GGCCTCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAAGAAGAAATGGAAACAGCCAA	2024
Query	1873	GAAAGGTCTCCTGGAACACGGCCGCAACTGGTCGGCCATCGCCCGGATGGTGGGCTCCAA	1932
Sbjct	2025	GAAAGGTCTCCTGGAACACGGCCGCAACTGGTCGGCCATCGCCCGGATGGTGGGCTCCAA	2084
Query	1933	GACTGTGTCGCAGTGTAAAGAACTTCTACTTCAACTACAAGAAGAGGCAGAACCTCGATGA	1992
Sbjct	2085	GACTGTGTCGCAGTGTAAAGAACTTCTACTTCAACTACAAGAAGAGGCAGAACCTCGATGA	2144
Query	1993	GATCTTGACAGCAGCACAAGCTGAAGATGGAGAAGGAGAGGAACGCGCGGAGGAAGAAGAA	2052
Sbjct	2145	GATCTTGACAGCAGCACAAGCTGAAGATGGAGAAGGAGAGGAACGCGCGGAGGAAGAAGAA	2204
Query	2053	GAAAGCGCCGGCGGCGGCCAGCGAGGAGGCTGCATTCCCGCCCGTGG	2099

|||||
Sbjct 2205 GAAAGCGCCGGCGCGGCCAGCGAGGAGGCTGCATTCCCGCCCGTGG 2251

Score = 154 bits (80), Expect = 2e-33
Identities = 80/80 (100%), Gaps = 0/80 (0%)
Strand=Plus/Plus

Query 2218 AGCCACTGTCAACAACAGCTCAGACACCGAGAGCATCCCCTCTCCTCACACTGAGGCCGC 2277

Sbjct 2319 AGCCACTGTCAACAACAGCTCAGACACCGAGAGCATCCCCTCTCCTCACACTGAGGCCGC 2378

Query 2278 CAAGGACACAGGGCAGAATG 2297

Sbjct 2379 CAAGGACACAGGGCAGAATG 2398

Score = 48.8 bits (25), Expect = 0.12
Identities = 27/28 (96%), Gaps = 0/28 (0%)
Strand=Plus/Plus

Query 2444 CCCTCTGCACCTCCTCCTGTGGTCCCCA 2471

Sbjct 2545 CCCTCTTCACCTCCTCCTGTGGTCCCCA 2572

CPU time: 0.05 user secs. 0.02 sys. secs 0.07 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 1177
Number of extensions: 44
Number of successful extensions: 7
Number of sequences better than 10.0: 1
Number of HSP's gapped: 5
Number of HSP's successfully gapped: 5
Length of query: 3094
Length of database: 17,886,619,220
Length adjustment: 27
Effective length of query: 3067

Effective length of database: 17,886,619,193

Effective search space: 54858261064931

Effective search space used: 54858261064931

X1: 11 (21.1 bits)

X2: 26 (50.0 bits)

X3: 26 (50.0 bits)

S1: 16 (31.5 bits)

S2: 22 (43.0 bits)